

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/303,232DATE: 05/10/1999
TIME: 15:29:15

Input Set: I303232.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

1 <110> Bayer Aktiengesellschaft
 2 <120> Nucleic acids which encode
 3 insect acetylcholine receptor subunits
 4 <130> Le A 33 020-Foreign Countries
 5 <140> US/09/303,232
 6 <141> 1999-04-30
 7 <150> DE-198 19 829.9
 8 <151> 1998-05-04
 E--> 9 <160> 6) 3 shown in file (see pp 7-18)
 10 <170> PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

Sequence 2 missing

E--> 11 <210> 3
 12 <211> 3701
 13 <212> DNA
 14 <213> Heliothis virescens
 15 <220>
 16 <221> CDS
 17 <222> (335) .. (1822)
 18 <400> 3
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 20 gccgtgactc cacacacatc ccctcggcgc agtaggcgtat gtttggaggat cggacggcac 120
 21 gcgtggccgt cggcgagcgg tcgtgaacaa gttgcataca tataaaaacc gtaaaaagat 180
 22 tgaattttaa gccgatcgtg ttgcatacat gctaatacag aagcgggagt gcggcggttg 240
 23 gtaggcgggg gtcgagtcgc gcggtcgggg gaaaatggcgc ggcgcggggc ggcggcggcgc 300
 24 gcgccgcgcg gcgccggcggc gtcgcggcgc tgac atg ggc ggg cgg gcg cgc ogc 355
 25 Met Gly Arg Ala Arg Arg
 26 1 5
 27 tcg cac ttg gcg gcg ccc ggc ctg ctg ctg ctg tgc ctg ctc 403
 28 Ser His Leu Ala Ala Pro Ala Gly Leu Leu Leu Leu Cys Leu Leu
 29 10 15 20
 30 tgg ccg agg ggg gca cgc tgc ggg tac cac gag aag cgg cta ctg cac 451
 31 Trp Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His
 32 25 30 35
 33 cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499
 34 His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu
 35 40 45 50 55
 36 agc gac ccg ctg cag ctc tcc ttc ggc ctc acg ctc atg cag atc atc 547
 37 Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
 38 60 65 70
 39 gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595

Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n-r Xaa.

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40	Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Lys			
41	75	80	85	
42	ctg gag tgg aat gat atg aac ttg agg tgg aac act tca gat ttc ggc	643		
43	Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Phe Gly			
44	90	95	100	
45	ggg gtc aaa gat tta aga gtg cca ccc cac aga cta tgg aaa cca gac	691		
46	Gly Val Lys Asp Leu Arg Val Pro Pro His Arg Leu Trp Lys Pro Asp			
47	105	110	115	
48	gtc ctt atg tac aac agc gcg gac gaa ggg ttc gac agc acg tat cca	739		
49	Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Ser Thr Tyr Pro			
50	120	125	130	135
51	acg aac gtg gtg gtg cgg aac aac ggc tcg tgt ctg tac gtg ccg ccc	787		
52	Thr Asn Val Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro			
53	140	145	150	
54	ggc atc ttc aag agc acc tgc aag atc gac atc acc tgg ttc ccc ttc	835		
55	Gly Ile Phe Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe			
56	155	160	165	
57	gac gac caa cga tgc gag atg aag ttt ggc agc tgg act tat gat ggt	883		
58	Asp Asp Gln Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly			
59	170	175	180	
60	tat cag ttg gat cta caa cta cag gat gaa ggg ggc gga gat ata agc	931		
61	Tyr Gln Leu Asp Leu Gln Leu Gln Asp Glu Gly Gly Asp Ile Ser			
62	185	190	195	
63	agt ttt gtc acg aat ggc gaa tgg gag tta ata gga gtc ccc ggc aag	979		
64	Ser Phe Val Thr Asn Gly Glu Trp Glu Leu Ile Gly Val Pro Gly Lys			
65	200	205	210	215
66	cgc aac gag atc tac tac aac tgt tgt ccg gag cca tac atc gac atc	1027		
67	Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile			
68	220	225	230	
69	acg ttt gcg gtg gtg atc cgg agg aaa acg ctc tac tac ttc ttc aat	1075		
70	Thr Phe Ala Val Val Ile Arg Arg Lys Thr Leu Tyr Tyr Phe Phe Asn			
71	235	240	245	
72	ctg atc gtg ccc tgc gtg ctc atc gcc tcc atg gct cta ttg ggg ttc	1123		
73	Leu Ile Val Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe			
74	250	255	260	
75	acc ttg cct cca gac tcc gga gaa aag ttg tct tta ggt gtg acg ata	1171		
76	Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile			
77	265	270	275	
78	tta ctg tcg ttg acg gtg ttc ctc aac atg gtg gcg gag acg atg cca	1219		
79	Leu Leu Ser Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro			
80	280	285	290	295
81	gcg acg tcg gac gcc gtg ccc ttg ctc ggc acc tac ttc aac tgc atc	1267		
82	Ala Thr Ser Asp Ala Val Pro Leu Leu Gly Thr Tyr Phe Asn Cys Ile			
83	300	305	310	
84	atg ttc atg gtg gct tcc tcc gtc gtc tcc acc ata ctg atc ctc aac	1315		
85	Met Phe Met Val Ala Ser Ser Val Val Ser Thr Ile Leu Ile Leu Asn			
86	315	320	325	
87	tac cac cac cgg cac gac act cac gaa atg agt gat tgg att cgt	1363		
88	Tyr His His Arg His Ala Asp Thr His Glu Met Ser Asp Trp Ile Arg			
89	330	335	340	

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RAW SEQUENCE LISTING
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90	tgc gtg ttc ctt tat tgg ctg ccg tgg gtg ctg cgc atg tca	cgg ccc	1411	
91	Cys Val Phe Leu Tyr Trp Leu Pro Trp Val Leu Arg Met Ser	Arg Pro		
92	345	350	355	
93	ggc tcg gcg acg acg ccg ccg ccg gcg cgc gta cct ccg	ccg ccg gac	1459	
94	Gly Ser Ala Thr Thr Pro Pro Pro Ala Arg Val Pro Pro Pro	Asp		
95	360	365	370	375
96	ctg gag ctg cgc gag ccg tcc tcc aag tcg ctc cta gcg aac	gtg ctc	1507	
97	Leu Glu Leu Arg Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn	Val Leu		
98	380	385	390	
99	gac atc gat gac gac ttc cgc cac ccg caa gcg cag cag	ccg caa tgc	1555	
100	Asp Ile Asp Asp Asp Phe Arg His Pro Gln Ala Gln Gln Pro	Gln Cys		
101	395	400	405	
102	tgc cga tac tac agg ggg ggt gag gag aat ggc gcg ggg	ttg gcg gcg	1603	
103	Cys Arg Tyr Tyr Arg Gly Gly Glu Glu Asn Gly Ala Gly	Leu Ala Ala		
104	410	415	420	
105	cac agt tgc ttc ggt gtc gac tac gag ctc tcc ctc att	ctg aag gag	1651	
106	His Ser Cys Phe Gly Val Asp Tyr Glu Leu Ser Leu Ile	Leu Lys Glu		
107	425	430	435	
108	att aga gtc atc aca gat cag atg cgc aag gac gac gaa	gat gcg gac	1699	
109	Ile Arg Val Ile Thr Asp Gln Met Arg Lys Asp Asp Glu	Asp Ala Asp		
110	440	445	450	455
111	att tcg cgc gac tgg aag ttc gcc gcc atg gtc gtg gac	aga ctg tgc	1747	
112	Ile Ser Arg Asp Trp Lys Phe Ala Ala Met Val Val Asp	Arg Leu Cys		
113	460	465	470	
114	ctt att atc ttt acc ctg ttc aca atc atc gcc acg cta	gcc gtg ctg	1795	
115	Leu Ile Ile Phe Thr Leu Phe Thr Ile Ile Ala Thr Leu	Ala Val Leu		
116	475	480	485	
117	ctg tcc gcg cca cac atc atg gtg tcg tagcgaccgc	cccgcttgcg	1842	
118	Leu Ser Ala Pro His Ile Met Val Ser			
119	490	495		
120	gatacgcatg cgaaaagttc tgtgataccg cgaatatttg ttaagttgtg	atgagcgaag	1902	
121	tggcgccgac ggtgacgccc cggcgctcga gttgccccc cctgcctcgc	cgcgcgcgc	1962	
122	ccccctgtaga cataagttac cgctgactgc caaccctgta cgttcaacaa	ataactgcgc	2022	
123	atccgactaa cgcttttat ccccttggaaa aattcagcga ttgtgtaccc	cttttttcca	2082	
124	agaataacaat gacaaatggt cgtcacgctc agtggaatca atccgtact	cttcgcggca	2142	
125	tattttccctt agggtatgtc acgagttga atgagcggtt ccgtatcaga	cgttccgtcc	2202	
126	ccggAACGGT cgccccctgc gataaaagtgg cagtagtgc tatacaggca	cttaaggccg	2262	
127	ccacgcccacg ggcggccggc ggcgtcgggc cggcaaccgc	cgaccctcac	2322	
128	ggccacccac tagacaagac tgcggcagaa aatatttgc	caaaaacgtc	2382	
129	ccgatgaacg acctgattcg cattttaaat taaaactttgt tagaacttct	tcgattcttg	2442	
130	aaatctattg tacagtttag agtttggcg gtgaaaacaat ggccctttgt	ttccttcttg	2502	
131	ttcgattcca tgaatcgtgg ttataatccc tagttttattt ttcggatata	tttgtgtcag	2562	
132	tagctagtat agaactttac aaacaatgtt gattcaattt	gtacaggttg tgatatgc	2622	
133	cgttgtaac gggtccgata ttgttataaa tggtaaaata cccatggcta	tagcttaata	2682	
134	aatcgttcgt taaaagttgt agttaaacaa atattatttt aataaagtca	tatctgggtc	2742	
135	ttccggAACG acttttacaa ataattaaat tacatattaa tatcacgtt	gtacttctt	2802	
136	ccatacagtt acagtaattc gtatgctgaa aataatatta	gcttgtaaaa	2862	
137	cgaaaattta ttcaaacaga tgcgaccatc gttcaaaaca	tttacatgt	2922	
138	catttataa gatataacaac attttataag tacaagaagt tgtaacatga	accggttttt	2982	
139	cgttacatag agggataac acaaagggtgc ctacatattt	acagatgcga	3042	

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140 gttgataaagc acaggtacac tatacctga catccgacag tcctgccgct cgtctgccac 3102
 141 actcgaaaac attcgacagt tcagttact gctccgcatt catcgattgt taagtttgg 3162
 142 gttctaactc atcgcattca tttcattcaa aaacattgtaa aacctctcaa ggggaaaacg 3222
 143 tggtaaac agtgagagtgc cgccgggtaca accgacacgcg gaatgtaccc tcgcaaggct 3282
 144 cctgtaatgt tttcctcttc cgagggtttg ctgagagtaa tcttagacgg tccgatggaa 3342
 145 gttgcggacc ggatatgatt acaagtcattt gtttttaagt catccgttta ttatttgtt 3402
 146 tatcttctta ccattcgcta gaggttgtgt gacgacccgg acgggtggcg ccccaacccg 3462
 147 cacacgcggg gttccatctt tgtatttagat ggaagttgtg cggcatctct cccgtcggcaa 3522
 148 tgggacaacc cgttgccttcc aacattgtt caattgttag gtttaactct gaattgcact 3582
 149 ttgtttatta aatataaaacg aatgaaacaa aaaaaaaaaaaaaaa aaaaaactcg agagtacttc 3642
 150 tagagcggcc gccccccat cgatttcca cccgggtggg gtaccargta agtgtaccc 3701

E--> 151 <210> 5
 152 <211> 3109
 153 <212> DNA
 154 <213> Heliothis virescens
 155 <220>
 156 <221> CDS
 157 <222> (95)..(1597)
 158 <400> 5

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 160 gtcgcgggt gtggtatgcc cgcgctcgcc cgct atg gcc cct atg ttg gcg gcc 115
 161 Met Ala Pro Met Leu Ala Ala
 162 1 5
 163 ttg gcg ctg ctg gct ttg ctg ccc gta tcg gag caa ggt cct cac gag 163
 164 Leu Ala Leu Leu Ala Leu Leu Pro Val Ser Glu Gln Gly Pro His Glu
 165 10 15 20
 166 aag aga ctc ctg aac gcg ttg ctg gcg aac tac aac acc ctg gag cga 211
 167 Lys Arg Leu Leu Asn Ala Leu Leu Ala Asn Tyr Asn Thr Leu Glu Arg
 168 25 30 35
 169 ccg gtg gcc aac gag agc gaa ccg cta gag gtc agg ttc ggc ttg acc 259
 170 Pro Val Ala Asn Glu Ser Glu Pro Leu Glu Val Arg Phe Gly Leu Thr
 171 40 45 50 55
 172 ttg cag caa atc att gac gtg gac gag aag aat caa cta ctt ata acc 307
 173 Leu Gln Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr
 174 60 65 70
 175 aat ata tgg ctg tcg ttg gag tgg aat gac tac aac ctg agg tgg aac 355
 176 Asn Ile Trp Leu Ser Leu Glu Trp Asn Asp Tyr Asn Leu Arg Trp Asn
 177 75 80 85
 178 gac agc gag tat ggc ggg gtc aag gac ctc agg atc acg ccc aac aag 403
 179 Asp Ser Glu Tyr Gly Gly Val Lys Asp Leu Arg Ile Thr Pro Asn Lys
 180 90 95 100
 181 ttg tgg aag ccg gac gtc ctt atg tat aat agt gct gac gag ggt ttt 451
 182 Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe
 183 105 110 115
 184 gac ggg acc tac cag acc aac gtg gtg gtc aga agc ggc ggc agt tgc 499
 185 Asp Gly Thr Tyr Gln Thr Asn Val Val Val Arg Ser Gly Gly Ser Cys
 186 120 125 130 135
 187 ctg tac gtg cca cct ggc ata ttc aag agc aca tgc aag atg gac atc 547
 188 Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Met Asp Ile

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RAW SEQUENCE LISTING

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Input Set: I303232.RAW

189	140	145	150	
190	gcg tgg ttt ccc ttc gac gac caa cac tgt gat atg aag ttc ggt agc			595
191	Ala Trp Phe Pro Phe Asp Asp Gln His Cys Asp Met Lys Phe Gly Ser			
192	155	160	165	
193	tgg aca tat gac ggc aat cag ttg gat ctg gtg cta aaa gat gag gca			643
194	Trp Thr Tyr Asp Gly Asn Gln Leu Asp Leu Val Leu Lys Asp Glu Ala			
195	170	175	180	
196	ggc ggc gat cta tcg gac ttc ata aca aat ggg gag tgg tat cta ata			691
197	Gly Gly Asp Leu Ser Asp Phe Ile Thr Asn Gly Glu Trp Tyr Leu Ile			
198	185	190	195	
199	gga atg cca ggc aaa aag aac aca ata aca tac gcg tgc tgc ccc gag			739
200	Gly Met Pro Gly Lys Lys Asn Thr Ile Thr Tyr Ala Cys Cys Pro Glu			
201	200	205	210	215
202	ccc tac gtg gac gtc acc ttc acc atc atg ata aga aga cga acc ttg			787
203	Pro Tyr Val Asp Val Thr Phe Thr Ile Met Ile Arg Arg Arg Thr Leu			
204	220	225	230	
205	tac tac ttc ttc aac ctg atc gtc ccg tgc gtg ctg atc tca tcg atg			835
206	Tyr Tyr Phe Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ser Ser Met			
207	235	240	245	
208	gca ctc ctc ggc ttc aca ctg cca cca gac tcc gga gag aaa ctc aca			883
209	Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Thr			
210	250	255	260	
211	ctt gga gtc act att ctt cta tcg ctg acg gtg ttc ctc aac ctg gta			931
212	Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn Leu Val			
213	265	270	275	
214	gcc gag acc ctg cca cag gtc tcc gac gct atc ccc ctg tta ggg acg			979
215	Ala Glu Thr Leu Pro Gln Val Ser Asp Ala Ile Pro Leu Leu Gly Thr			
216	280	285	290	295
217	tac ttc aat tgc atc atg ttc atg gta gcg tgc tct gtg gta ctg act			1027
218	Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val Leu Thr			
219	300	305	310	
220	gtg gtg gta ctc aat tac cac cat cga aca gct gat ata cat gaa atg			1075
221	Val Val Val Leu Asn Tyr His His Arg Thr Ala Asp Ile His Glu Met			
222	315	320	325	
223	cca cag tgg ata aaa tca gta ttc cta caa tgg ttg cca tgg ata ctg			1123
224	Pro Gln Trp Ile Lys Ser Val Phe Leu Gln Trp Leu Pro Trp Ile Leu			
225	330	335	340	
226	cga atg tcg agg cca ggg aag aag atc acc agg aag act ata atg atg			1171
227	Arg Met Ser Arg Pro Gly Lys Lys Ile Thr Arg Lys Thr Ile Met Met			
228	345	350	355	
229	aac acg agg atg agg gag ctg gaa ctg aag gag agg tcg tcg aag tcc			1219
230	Asn Thr Arg Met Arg Glu Leu Glu Leu Lys Glu Arg Ser Ser Lys Ser			
231	360	365	370	375
232	ttg ctg gcg aat gtt cta gat att gat gat gac ttc aga cac ggc cct			1267
233	Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Gly Pro			
234	380	385	390	
235	ccg cct cct aac agt act gcc tcg acc ggg aat ttg gga cct ggg tgc			1315
236	Pro Pro Pro Asn Ser Thr Ala Ser Thr Gly Asn Leu Gly Pro Gly Cys			
237	395	400	405	
238	tca ata ttc cgc acg gat ttc cgt cgg tcg ttc gtc cgt ccg tcc acg			1363

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/303,232

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delete at end of file

~~SEQUENCE LISTING~~

delete - do not use?
under new
Sequence Rules

<110> Bayer Aktiengesellschaft

<120> Nucleic acids which encode
insect acetylcholine receptor subunits

<130> Le A 33 020-Foreign Countries

<140> 09/303 232

<141> 1999-04-30 ← odd date, how about

a serial number

for been

assigned

<150> DE-198 19 829.9

<151> 1998-05-04

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 2886

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (372) .. (2681)

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aaacaataaa gcatatactt gccatattga tataaaggga aatcgtaaa aggccgtgaa 180

aatttcgtaa gattagttgg tattaaggc agcccatgca cacagctaaa aagggaaacta 240

aaaaaacccc gcacagaaca atgaaagctg cagcagctgg ataaggccga caaaaccgaa 300

aatttatatta ttgtaatcta gtagagagca gacaacatat ccgctggcaa caaccaacac 360

cgaaagagac t atg aaa aat gca caa ctg aaa ctg act gaa gtt gac gat 410

Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp

1 5 10

gat gag ctg tgg ctg gca gta aga tta gcg cac tgc agc agc aac ttt 458

Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe

15

20

25

agc agc agt agc agc aca aga acc acc agc agc aac cag agg cac aac 506

Ser Ser Ser Ser Thr Arg Thr Ser Ser Asn Gln Arg His Asn

30

35

40

45

cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac 554

Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His

50

55

60

agc aac att gca agc gag cag cac aat agc cag caa cag gag cca gca 602

Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Glu Pro Ala

65

70

75

This is a
print of the entire
file - file was
printed for explanatory
purposes.

tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag		650
Ser Lys Asp Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln		
80 85 90		
acg cat ctg caa cag cta gac agc agc aac atg ttg tcg cca aag aca		698
Thr His Leu Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr		
95 100 105		
gcc gca gca gca act gct gcc ggc gat gaa gca aca acc caa caa cca		746
Ala Ala Ala Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro		
110 115 120 125		
aca aac ata aga ctg tgt gca cgc aag cga caa cga ttg cgt cgc cga		794
Thr Asn Ile Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg		
130 135 140		
cga aaa aga aaa cca gca acc cca aac gaa aca gat atc aag aaa caa		842
Arg Lys Arg Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln		
145 150 155		
cag caa ctt agc atg cct ccc ttc aaa acg cgc aaa tcc acg gac acc		890
Gln Gln Leu Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr		
160 165 170		
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Tyr Ser Thr Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met		
175 180 185		
caa tgt cga gcc agc gac aat gag ttc agt att ccg ata tcg aga cat		986
Gln Cys Arg Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His		
190 195 200 205		
gat aga gta tcc acg gcc aca ttc gcc tgg gtg ttg cat gtg ctg cag		1034
Asp Arg Val Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln		
210 215 220		
gtg ctg ctc gtg tcg ctg caa cag tgg caa ctt cac gtg caa cag cga		1082
Val Leu Leu Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg		
225 230 235		
tcg gtg cta ctg ttc aga agg atc gca gcg agc acc atc gcc ttc att		1130
Ser Val Leu Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile		
240 245 250		
tcc tat tta ggc agc ttt gca gcg caa ctg aaa aat agc agc agc agc		1178
Ser Tyr Leu Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser		
255 260 265		
agt agc agc aac agc agc aac aac agc agc agc agc caa ata tta aac		1226
Ser Ser Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn		
270 275 280 285		
gga ctt aat aaa cac tca tgg ata ttt tta ttg ata tat ttg aat tta		1274
Gly Leu Asn Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu		
290 295 300		
tct gct aaa gtt tgc cta gca gga tat cat gaa aag aga ctg tta cac		1322
Ser Ala Lys Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His		
305 310 315		

gat ctt ttg gat cct tat aat aca cta gaa cgt ccc gtt ctc aat gaa		1370
Asp Leu Leu Asp Pro Tyr Asn Thr Leu Glu Arg Pro Val Leu Asn Glu		
320 325 330		
tcg gac ccg tta caa tta agc ttt ggt tta act tta atg caa att atc		1418
Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile		
335 340 345		
gat gtg gac gag aaa aat caa ttg cta gtc act aat gtg tgg tta aaa		1466
Asp Val Asp Glu Lys Asn Gln Leu Leu Val Thr Asn Val Trp Leu Lys		
350 355 360 365		
ctg gag tgg aac gac atg aat ctc cgc tgg aac acc tcc gac tat ggc		1514
Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Tyr Gly		
370 375 380		
gga gtt aag gat ctg cga ata ccg ccg cat cgc atc tgg aag ccg gac		1562
Gly Val Lys Asp Leu Arg Ile Pro Pro His Arg Ile Trp Lys Pro Asp		
385 390 395		
gtg ctg atg tac aac agt gcg gat gag gga ttt gac ggc acc tac cag		1610
Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln		
400 405 410		
acg aac gtg gtg gtg cgaa aac aac ggc tcg tgt cta tac gtt ccg ccg		1658
Thr Asn Val Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro		
415 420 425		
ggg atc ttc aag tcg acg tgc aag atc gac atc acg tgg ttc ccc ttc		1706
Gly Ile Phe Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe		
430 435 440 445		
gat gac cag ccg tgc gag atg aag ttc ggc agt tgg acc tac gac gga		1754
Asp Asp Gln Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly		
450 455 460		
ttc cag ctg gat tta caa tta caa gat gaa act ggc ggt gat atc agc		1802
Phe Gln Leu Asp Leu Gln Leu Asp Glu Thr Gly Gly Asp Ile Ser		
465 470 475		
agt tac gtg ctc aac ggc gag tgg gaa cta ctg ggt gtg ccc ggc aaa		1850
Ser Tyr Val Leu Asn Gly Glu Trp Glu Leu Leu Gly Val Pro Gly Lys		
480 485 490		
cgt aac gag atc tat tac aac tgc tgc ccg gaa ccc tat ata gac atc		1898
Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile		
495 500 505		
acc ttc gcc atc atc atc cgc cga cga aca ctg tac tat ttc ttc aac		1946
Thr Phe Ala Ile Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn		
510 515 520 525		
ctg atc ata cct tgt gta ctg att gcc tcc atg gcc ttg ctc gga ttc		1994
Leu Ile Ile Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe		
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acc ctg ccg cca gat tcg ggt gaa aaa tta tcg ctg ggt gtt acc atc		2042
Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile		
545 550 555		

10

ttg ctc tcg ctg acc gtg ttt ctg aat atg gtt gcc gag aca atg ccg Leu Leu Ser Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro 560 565 570	2090
gct act tcc gat gcg gtg cca ttg tgg ata cgc atc gtg ttt ttg tgc Ala Thr Ser Asp Ala Val Pro Leu Trp Ile Arg Ile Val Phe Leu Cys 575 580 585	2138
tgg ctg cca tgg ata ttg cga atg agt cgc cca gga cga ccg ctg atc Trp Leu Pro Trp Ile Leu Arg Met Ser Arg Pro Gly Arg Pro Leu Ile 590 595 600 605	2186
cta gag ttc ccg acc acg ccc tgt tcg gac aca tcc tcc gag cg ^g aag Leu Glu Phe Pro Thr Thr Pro Cys Ser Asp Thr Ser Ser Glu Arg Lys 610 615 620	2234
cac cag ata ctc tcc gac gtt gag ctg aaa gag cgc tcg tcg aaa tcg His Gln Ile Leu Ser Asp Val Glu Leu Lys Glu Arg Ser Ser Lys Ser 625 630 635	2282
ctg ctg gcc aac gta cta gac atc gat gat gac ttc cgg cac aat tgt Leu Leu Ala Asn Val Ile Asp Ile Asp Asp Asp Phe Arg His Asn Cys 640 645 650	2330
cg ^c ccc atg acg ccc ggc gga aca ctg cca cac aac ccg gct ttc tat Arg Pro Met Thr Pro Gly Gly Thr Leu Pro His Asn Pro Ala Phe Tyr 655 660 665	2378
cg ^c acg gtt tat gga caa ggc gac gat ggc agc att ggg cca att ggc Arg Thr Val Tyr Gly Gln Gly Asp Asp Gly Ser Ile Gly Pro Ile Gly 670 675 680 685	2426
agc acc cga atg ccg gat gcg gtc acc cat cat acg tcg atc aaa tca Ser Thr Arg Met Pro Asp Ala Val Thr His His Thr Cys Ile Lys Ser 690 695 700	2474
tca act gaa tat gaa tta ggt tta atc tta aag gaa att cg ^c ttt ata Ser Thr Glu Tyr Glu Leu Gly Leu Ile Leu Lys Glu Ile Arg Phe Ile 705 710 715	2522
act gat cag cta cgt aaa gat gac gag tcg aat gac att gcc aat gat Thr Asp Gln Leu Arg Lys Asp Asp Glu Cys Asn Asp Ile Ala Asn Asp 720 725 730	2570
tgg aaa ttt gca gct atg gtc gtt gac aga ctg tcg ctt atc ata ttc Trp Lys Phe Ala Ala Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe 735 740 745	2618
aca atg ttc gca ata tta gcc aca ata gct gta cta cta tcg gca cca Thr Met Phe Ala Ile Leu Ala Thr Ile Ala Val Leu Leu Ser Ala Pro 750 755 760 765	2666
cat att att gtc tcg tagccatatg gg ^c gaggtgg ttattgttat tggtttatt His Ile Ile Val Ser 770	2721
ataaaaatcaa tttgttaatt attaaattaa taacgaaact cttaagttaa attaaaacta aaaagacact aaaaaagcac aaaaaaatag gaaaatacat gataaaaccc atgaactaaa	2781 2841

taatacatcc aagaaaaacc aaaacaaaaaa aaaaaaaaaaaa aaaaaa

2886

11

where is Sequence 2? per legend
Riley ... the sequence identifier
shall begin with 1
and increase sequentially
by integers. If 3

<210> 3
<211> 3701
<212> DNA
<213> Heliothis virescens

<220>
<221> CDS
<222> (335)..(1822)

<400> 3

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gcgtggccgt cgccgagcgg tcgtgaacaa gttgcataca tatgaaaacc gtaaaaagat 180

tgaattttaa gccgatcgtg ttgcatacatc cctaatacgag aagcgggagt gcggcggttg 240

gtaggcgggg gtcgagtcgc gcggtcggg gaaatggcgc ggccggggc ggccggcggcg 300

gcggcgcgcg gcgcggcggc gtcgcggcgc tgac atg ggc ggg cgg gcg cgc cgc 355

Met Gly Gly Arg Ala Arg Arg
1 5

tcg cac ttg gcg gcg ccc gcg ggc ctg ctg ctg ctg tgc ctg ctc 403
Ser His Leu Ala Ala Pro Ala Gly Leu Leu Leu Leu Cys Leu Leu

10 15 20

tgg ccg agg ggg gca cgc tgc ggg tac cac gag aag cgg cta ctg cac 451
Trp Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His
25 30 35

cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499
His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu
40 45 50 55

agc gac ccg ctg cag ctc tcc ttc ggc ctc acg ctc atg cag atc atc 547
Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
60 65 70

gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595
Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Lys
75 80 85

cta gag tgg aat gat atg aac ttg agg tgg aac act tca gat ttc ggc 643
Leu Glu Trp Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Phe Gly
90 95 100

ggg gtc aaa gat tta aga gtg cca ccc cac aga cta tgg aaa cca gac 691
Gly Val Lys Asp Leu Arg Val Pro Pro His Arg Leu Trp Lys Pro Asp
105 110 115

Sequence
only are
in the
file, please
number
them

1, 2, 3.

gtc ctt atg tac aac agc gcg gac gaa ggg ttc gac agc acg tat cca		739
Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Ser Thr Tyr Pro		
120 125 130 135		
acg aac gtg gtg cggtt aac aac ggc tcgttgt ctgtac gtg ccgc ccc		787
Thr Asn Val Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro		
140 145 150		
ggc atc ttc aag agc acc tgc aag atc gac atc acc tgg ttc ccc ttc		835
Gly Ile Phe Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe		
155 160 165		
gac gac caa cga tgc gag atg aag ttt ggc agc tgg act tat gat ggt		883
Asp Asp Gln Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly		
170 175 180		
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Tyr Gln Leu Asp Leu Gln Leu Asp Glu Gly Gly Asp Ile Ser		
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Ser Phe Val Thr Asn Gly Glu Trp Glu Leu Ile Gly Val Pro Gly Lys		
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cgc aac gag atc tac tac aac tgt tgc ccg gag cca tac atc gac atc		1027
Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile		
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Thr Phe Ala Val Val Ile Arg Arg Lys Thr Leu Tyr Tyr Phe Phe Asn		
235 240 245		
ctg atc gtg ccc tgc gtg ctc atc gcc tcc atg gct cta ttg ggg ttc		1123
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Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile		
265 270 275		
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Ala Thr Ser Asp Ala Val Pro Leu Leu Gly Thr Tyr Phe Asn Cys Ile		
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Met Phe Met Val Ala Ser Ser Val Val Ser Thr Ile Leu Ile Leu Asn		
315 320 325		
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Tyr His His Arg His Ala Asp Thr His Glu Met Ser Asp Trp Ile Arg		
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Cys Val Phe Leu Tyr Trp Leu Pro Trp Val Leu Arg Met Ser Arg Pro		
345 350 355		

ggc tcg gcg acg acg ccg ccg gcg cgc gta cct ccg ccg ccg gac 1459
 Gly Ser Ala Thr Thr Pro Pro Pro Ala Arg Val Pro Pro Pro Pro Asp
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 380 385 390

gac atc gat gac gac ttc cgc cac ccg caa gcg cag cag ccg caa tgc 1555
 Asp Ile Asp Asp Asp Phe Arg His Pro Gln Ala Gln Gln Pro Gln Cys
 395 400 405

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 Cys Arg Tyr Tyr Arg Gly Gly Glu Glu Asn Gly Ala Gly Leu Ala Ala
 410 415 420

cac agt tgc ttc ggt gtc gac tac gag ctc tcc ctc att ctg aag gag 1651
 His Ser Cys Phe Gly Val Asp Tyr Glu Leu Ser Leu Ile Leu Lys Glu
 425 430 435

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 Ile Arg Val Ile Thr Asp Gln Met Arg Lys Asp Asp Glu Asp Ala Asp
 440 445 450 455

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 490 495

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 ttgtttatta aatataaACG aatgaaacAA aaaaaaaaaa aaaaaactcg agagtacttc 3642
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Where's sequence 4?

<210> 5
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 <212> DNA
 <213> Heliothis virescens

<220>
 <221> CDS
 <222> (95)..(1597)

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Met Ala Pro Met Leu Ala Ala
1 5

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Lys	Arg	Leu	Leu	Asn	Ala	Leu	Leu	Ala	Asn	Tyr	Asn	Thr	Leu	Glu	Arg	
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Pro	Val	Ala	Asn	Glu	Ser	Glu	Pro	Leu	Glu	Val	Arg	Phe	Gly	Leu	Thr	
40					45					50			55			
ttg	cag	caa	atc	att	gac	gtg	gac	gag	aag	aat	caa	cta	ctt	ata	acc	307
Leu	Gln	Gln	Ile	Ile	Asp	Val	Asp	Glu	Lys	Asn	Gln	Leu	Leu	Ile	Thr	
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aat	ata	tgg	ctg	tcg	ttg	gag	tgg	aat	gac	tac	aac	ctg	agg	tgg	aac	355
Asn	Ile	Trp	Leu	Ser	Leu	Glu	Trp	Asn	Asp	Tyr	Asn	Leu	Arg	Trp	Asn	
75					80					85						
gac	agc	gag	tat	ggc	ggg	gtc	aag	gac	ctc	agg	atc	acg	ccc	aac	aag	403
Asp	Ser	Glu	Tyr	Gly	Gly	Val	Lys	Asp	Leu	Arg	Ile	Thr	Pro	Asn	Lys	
90					95					100						
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Leu	Trp	Lys	Pro	Asp	Val	Leu	Met	Tyr	Asn	Ser	Ala	Asp	Glu	Gly	Phe	
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Ala	Trp	Phe	Pro	Phe	Asp	Asp	Gln	His	Cys	Asp	Met	Lys	Phe	Gly	Ser	
155					160					165						
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Tyr	Tyr	Phe	Phe	Asn	Leu	Ile	Val	Pro	Cys	Val	Leu	Ile	Ser	Ser	Met	
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		250				255						260				
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Leu	Gly	Val	Thr	Ile	Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Asn	Leu	Val	
		265				270						275				
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Ala	Glu	Thr	Leu	Pro	Gln	Val	Ser	Asp	Ala	Ile	Pro	Leu	Leu	Gly	Thr	
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Tyr	Phe	Asn	Cys	Ile	Met	Phe	Met	Val	Ala	Ser	Ser	Val	Val	Leu	Thr	
		300				305								310		
gtg	gtg	gta	ctc	aat	tac	cac	cat	cga	aca	gct	gat	ata	cat	gaa	atg	1075
Val	Val	Val	Leu	Asn	Tyr	His	His	Arg	Thr	Ala	Asp	Ile	His	Glu	Met	
		315				320						325				
cca	cag	tgg	ata	aaa	tca	gta	tcc	cta	caa	tgg	ttg	cca	tgg	ata	ctg	1123
Pro	Gln	Trp	Ile	Lys	Ser	Val	Phe	Leu	Gln	Trp	Leu	Pro	Trp	Ile	Leu	
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cga	atg	tcg	agg	cca	ggg	aag	aag	atc	acc	agg	aag	act	ata	atg	atg	1171
Arg	Met	Ser	Arg	Pro	Gly	Lys	Lys	Ile	Thr	Arg	Lys	Thr	Ile	Met	Met	
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Asn	Thr	Arg	Met	Arg	Glu	Leu	Glu	Leu	Lys	Glu	Arg	Ser	Ser	Lys	Ser	
		360			365					370				375		
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Met	Glu	Asp	Val	Gly	Gly	Leu	Gly	Ser	His	His	Arg	Glu	Leu	His		
		425			430							435				
ctc	ata	ctg	aga	gag	ctg	cag	tcc	atc	acg	gcc	agg	atg	aag	aag	gct	1459
Leu	Ile	Leu	Arg	Glu	Leu	Gln	Phe	Ile	Thr	Ala	Arg	Met	Lys	Lys	Ala	
		440			445							450			455	
gat	gag	gaa	gcc	gag	ctg	atc	agc	gac	tgg	aag	ttt	gct	gcg	atg	gtt	1507
Asp	Glu	Glu	Ala	Glu	Leu	Ile	Ser	Asp	Trp	Lys	Phe	Ala	Ala	Met	Val	
		460			465							470				
ttt	gtt	gat	agg	ttt	tgc	ctg	tcc	gtg	tcc	aca	ctt	ttc	aca	atc	atc	1555

Val Asp Arg Phe Cys Leu Phe Val Phe Thr Leu Phe Thr Ile Ile Ala
 475 480 485

aca gta gct gtc ctg tta tcg gca ccg cat atc atc gtg caa 1597
 Thr Val Ala Val Leu Leu Ser Ala Pro His Ile Ile Val Gln
 490 495 500

tgaaccaacc actgagccgg caactccggc gcatgaatga gagaaataat tattagatcg 1657
 ccgatttgta attataattg ataatgtaat taaattaaat acgtgggtga aacgcacacg 1717
 tctccataac aaagtcttaa gacattaaat tatgataaaat ttacatattg tagttaagtc 1777
 gagtgttgc 1837
 tcttattgtt gtatattgta tcgttgc 1897
 gtttgc 1957
 taaaacaat gtgatgttgc 2017
 taaaataaa caatattaat tactattact aaacgatatt ataaacgaag tactaacgag 2077
 gtttgc 2137
 attacggaaa aaagtttatt gaaaattgaa cttttggaa ggaaagtaac gtttgc 2197
 aaaagttgt aaaacgaaag ttcgggtcg 2257
 tattaggaa aagaaggcc 2317
 aatgagggat cacagatgat gacaaaaaac cttagggtat ataagtaatg tacataatgg 2377
 atcaaatac ggttagtca agaatagttt acgatttaag attattccat tcgatattaa 2437
 aattcgatta gcgattgtcg ctgcgtctac tttgatacat atcgatttgc 2497
 tataaatttgc 2557
 aatgtactac gaagattttt tccaggaatt gttttttttt 2617
 aacaattaat acggaaacca 2677
 taaatttgc 2737
 ctcattgtcg attaaatggc 2797
 actatcgata gcgtaatatt 2857
 tcagaaatag tcattaattt ggaatcggtt 2917
 acaatgctgt tgatatcact aaccatcacg 2977
 tattgcggc 3037
 tacttctaga gcggccgcgg 3097
 tacccaatttgc 3109

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